

## SEQUENCE LISTING

<110> Shone, Clifford Charles  
Sutton, John Mark

<120> Targeted Agents for Nerve Regeneration

<130> MSQ01-003-US

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<151> 2002-07-19

<160> 27

<170> PatentIn version 3.1

<210> 1

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1

Ile Glu Gly Arg Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile  
1 5 10 15

Asp Gln Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu  
20 25 30

Ser Lys Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser  
35 40 45

Glu Ile Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe  
50 55 60

Pro Ser Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn  
65 70 75 80

Lys Met Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro  
85 90 95

Ala Tyr Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly  
100 105 110

Thr Ile Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Phe Leu Asn  
115 120 125

Lys Asp Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val  
130 135 140

Ser Gln Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys  
 145 150 155 160

Gly Ser Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln  
 165 170 175

Leu Glu Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met  
 180 185 190

Arg Leu Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met  
 195 200 205

Gly Thr Ala Ile Asn Pro Lys  
 210 215

<210> 2

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2

Ala Glu Thr Lys Asn Phe Thr Asp Leu Val Glu Ala Thr Lys Trp Gly  
 1 5 10 15

Asn Ser Leu Ile Lys Ser Ala Lys Tyr Ser Ser Lys Asp Lys Met Ala  
 20 25 30

Ile Tyr Asn Tyr Thr Lys Asn Ser Ser Pro Ile Asn Thr Pro Leu Arg  
 35 40 45

Ser Ala Asn Gly Asp Val Asn Lys Leu Ser Glu Asn Ile Gln Glu Gln  
 50 55 60

Val Arg Gln Leu Asp Ser Thr Ile Ser Lys Ser Val Thr Pro Asp Ser  
 65 70 75 80

Val Tyr Val Tyr Arg Leu Leu Asn Leu Asp Tyr Leu Ser Ser Ile Thr  
 85 90 95

Gly Phe Thr Arg Glu Asp Leu His Met Leu Gln Gln Thr Asn Asn Gly  
 100 105 110

Gln Tyr Asn Glu Ala Leu Val Ser Lys Leu Asn Asn Leu Met Asn Ser  
 115 120 125

Arg Ile Tyr Arg Glu Asn Gly Tyr Ser Ser Thr Gln Leu Val Ser Gly  
 130 135 140

Ala Ala Leu Ala Gly Arg Pro Ile Glu Leu Lys Leu Glu Leu Pro Lys  
 145 150 155 160

Gly Thr Lys Ala Ala Tyr Ile Asp Ser Lys Glu Leu Thr Ala Tyr Pro  
 165 170 175

Gly Gln Gln Glu Val Leu Leu Pro Arg Gly Thr Glu Tyr Ala Val Gly  
 180 185 190

Ser Val Lys Leu Ser Asp Asn Lys Arg Lys Ile Ile Ile Thr Ala Val  
 195 200 205

Val Phe Lys Lys  
 210

<210> 3

<211> 636

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 3

Gly Cys Thr Gly Ala Ala Ala Cys Cys Ala Ala Ala Ala Ala Cys Thr  
 1 5 10 15

Thr Cys Ala Cys Cys Gly Ala Cys Cys Thr Gly Gly Thr Thr Gly Ala  
 20 25 30

Ala Gly Cys Thr Ala Cys Cys Ala Ala Ala Thr Gly Gly Gly Thr  
 35 40 45

Ala Ala Cys Thr Cys Thr Cys Thr Gly Ala Thr Cys Ala Ala Ala Thr  
 50 55 60

Cys Thr Gly Cys Thr Ala Ala Ala Thr Ala Cys Thr Cys Thr Thr Cys  
 65 70 75 80

Thr Ala Ala Ala Gly Ala Cys Ala Ala Ala Ala Thr Gly Gly Cys Thr  
 85 90 95

Ala Thr Cys Thr Ala Cys Ala Ala Cys Thr Ala Cys Ala Cys Cys Ala  
 100 105 110

Ala Ala Ala Ala Cys Thr Cys Thr Cys Thr Cys Cys Gly Ala Thr  
 115 120 125

Cys Ala Ala Cys Ala Cys Cys Cys Gly Cys Thr Gly Cys Gly Thr

130

135

140

Thr Cys Thr Gly Cys Thr Ala Ala Cys Gly Gly Thr Gly Ala Cys Gly  
 145 150 155 160

Thr Thr Ala Ala Cys Ala Ala Ala Cys Thr Gly Thr Cys Thr Gly Ala  
 165 170 175

Ala Ala Ala Cys Ala Thr Cys Cys Ala Gly Gly Ala Ala Cys Ala Gly  
 180 185 190

Gly Thr Thr Cys Gly Thr Cys Ala Gly Cys Thr Gly Gly Ala Cys Thr  
 195 200 205

Cys Thr Ala Cys Cys Ala Thr Cys Thr Cys Thr Ala Ala Ala Thr Cys  
 210 215 220

Thr Gly Thr Thr Ala Cys Cys Cys Gly Gly Ala Cys Thr Cys Thr  
 225 230 235 240

Gly Thr Thr Thr Ala Cys Gly Thr Thr Thr Ala Cys Cys Gly Thr Cys  
 245 250 255

Thr Gly Cys Thr Gly Ala Ala Cys Cys Thr Gly Gly Ala Cys Thr Ala  
 260 265 270

Cys Cys Thr Gly Thr Cys Thr Cys Thr Ala Thr Cys Ala Cys Cys  
 275 280 285

Gly Gly Thr Thr Thr Cys Ala Cys Cys Cys Gly Thr Gly Ala Ala Gly  
 290 295 300

Ala Cys Cys Thr Gly Cys Ala Cys Ala Thr Gly Cys Thr Gly Cys Ala  
 305 310 315 320

Gly Cys Ala Gly Ala Cys Cys Ala Ala Cys Ala Ala Cys Gly Gly Thr  
 325 330 335

Cys Ala Gly Thr Ala Cys Ala Ala Cys Gly Ala Ala Gly Cys Thr Cys  
 340 345 350

Thr Gly Gly Thr Thr Cys Thr Ala Ala Ala Cys Thr Gly Ala Ala  
 355 360 365

Cys Ala Ala Cys Cys Thr Gly Ala Thr Gly Ala Ala Cys Thr Cys Thr  
 370 375 380

Cys Gly Thr Ala Thr Cys Thr Ala Cys Cys Gly Thr Gly Ala Ala Ala

385

390

395

400

Ala Cys Gly Gly Thr Thr Ala Cys Thr Cys Thr Thr Cys Thr Ala Cys  
405 410 415

Cys Cys Ala Gly Cys Thr Gly Gly Thr Thr Thr Cys Thr Gly Gly Thr  
420 425 430

Gly Cys Thr Gly Cys Thr Cys Thr Gly Gly Cys Thr Gly Gly Thr Cys  
435 440 445

Gly Thr Cys Cys Gly Ala Thr Cys Gly Ala Ala Cys Thr Gly Ala Ala  
450 455 460

Ala Cys Thr Gly Gly Ala Ala Cys Thr Gly Cys Cys Gly Ala Ala Ala  
465 470 475 480

Gly Gly Thr Ala Cys Cys Ala Ala Ala Gly Cys Thr Gly Cys Thr Thr  
485 490 495

Ala Cys Ala Thr Cys Gly Ala Cys Thr Cys Thr Ala Ala Ala Gly Ala  
500 505 510

Ala Cys Thr Gly Ala Cys Cys Gly Cys Thr Thr Ala Cys Cys Cys Cys  
515 520 525

Gly Gly Thr Cys Ala Gly Cys Ala Gly Gly Ala Ala Gly Thr Thr Cys  
530 535 540

Thr Gly Cys Thr Gly Cys Cys Gly Cys Gly Thr Gly Gly Thr Ala Cys  
545 550 555 560

Cys Gly Ala Ala Thr Ala Cys Gly Cys Thr Gly Thr Thr Gly Gly Thr  
565 570 575

Thr Cys Thr Gly Thr Thr Ala Ala Ala Cys Thr Gly Thr Cys Thr Gly  
580 585 590

Ala Cys Ala Ala Cys Ala Ala Ala Cys Gly Thr Ala Ala Ala Ala Thr  
595 600 605

Cys Ala Thr Cys Ala Thr Cys Ala Cys Cys Gly Cys Thr Gly Thr Thr  
610 615 620

Gly Thr Thr Thr Thr Cys Ala Ala Gly Ala Ala Gly  
625 630 635

<211> 212  
 <212> PRT  
 <213> *Staphylococcus aureus*  
 <400> 4

Ala Asp Val Lys Asn Phe Thr Asp Leu Asp Glu Ala Thr Lys Trp Gly  
 1 5 10 15

Asn Lys Leu Ile Lys Gln Ala Lys Tyr Ser Ser Asp Asp Lys Ile Ala  
 20 25 30

Leu Tyr Glu Tyr Thr Lys Asp Ser Ser Lys Ile Asn Gly Pro Leu Arg  
 35 40 45

Leu Ala Gly Gly Asp Ile Asn Lys Leu Asp Ser Thr Thr Gln Asp Lys  
 50 55 60

Val Arg Arg Leu Asp Ser Ser Ile Ser Lys Ser Thr Thr Pro Glu Ser  
 65 70 75 80

Val Tyr Val Tyr Arg Leu Leu Asn Leu Asp Tyr Leu Thr Ser Ile Val  
 85 90 95

Gly Phe Thr Asn Glu Asp Leu Tyr Lys Leu Gln Gln Thr Asn Asn Gly  
 100 105 110

Gln Tyr Asp Glu Asn Leu Val Arg Lys Leu Asn Asn Val Met Asn Ser  
 115 120 125

Arg Ile Tyr Arg Glu Asp Gly Tyr Ser Ser Thr Gln Leu Val Ser Gly  
 130 135 140

Ala Ala Val Gly Gly Arg Pro Ile Glu Leu Arg Leu Glu Leu Pro Lys  
 145 150 155 160

Gly Thr Lys Ala Ala Tyr Leu Asn Ser Lys Asp Leu Thr Ala Tyr Tyr  
 165 170 175

Gly Gln Gln Glu Val Leu Leu Pro Arg Gly Thr Glu Tyr Ala Val Gly  
 180 185 190

Ser Val Glu Leu Ser Asn Asp Lys Lys Ile Ile Ile Thr Ala Ile  
 195 200 205

Val Phe Lys Lys  
 210

<210> 5  
 <211> 247  
 <212> PRT

<213> *Staphylococcus aureus*  
 <400> 5

Met Lys Arg Lys Leu Phe Phe Lys Ile Ile Phe Val Leu Ser Leu Val  
 1 5 10 15

Leu Ser Ile His Ser Ile Asn Asp Arg Thr Thr Glu Leu Ser Asn Ile  
 20 25 30

Ala Leu Ala Asp Asp Val Lys Asn Phe Thr Asp Leu Thr Glu Ala Thr  
 35 40 45

Asn Trp Gly Asn Lys Leu Ile Lys Gln Ala Asn Tyr Ser Ser Lys Asp  
 50 55 60

Lys Glu Ala Ile Tyr Asn Tyr Thr Lys Tyr Ser Ser Pro Ile Asn Thr  
 65 70 75 80

Pro Leu Arg Ser Ser Gln Gly Asp Ile Ser Asn Phe Ser Ala Asp Leu  
 85 90 95

Gln Glu Lys Ile Leu Arg Leu Asp Arg Leu Ile Ser Lys Ser Ser Thr  
 100 105 110

Ser Asp Ser Val Tyr Val Tyr Arg Leu Leu Asn Leu Asp Tyr Leu Ser  
 115 120 125

Ser Val Lys Gly Phe Ser Ser Glu Asp Leu Glu Leu Leu Tyr Lys Thr  
 130 135 140

Glu Asn Gly Lys Tyr Asn Glu Glu Leu Val Lys Lys Leu Asn Asn Ile  
 145 150 155 160

Met Asn Ser Lys Ile Tyr Thr Glu Tyr Gly Tyr Ser Ser Thr Gln Leu  
 165 170 175

Val Lys Gly Ala Ala Leu Ala Gly Arg Pro Ile Glu Leu Lys Leu Gln  
 180 185 190

Leu Pro Lys Gly Thr Lys Ala Ala Tyr Ile Asp Ser Lys Asn Leu Thr  
 195 200 205

Ala Tyr Pro Gly Gln Gln Glu Ile Leu Leu Pro Arg Gly Thr Asp Tyr  
 210 215 220

Thr Ile Asn Thr Val Lys Leu Ser Asp Asp His Lys Arg Ile Leu Ile  
 225 230 235 240

Glu Gly Ile val Phe Lys Lys

<210> 6  
 <211> 211  
 <212> PRT  
 <213> Clostridium limosum  
 <400> 6

Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln Ala Lys  
 1 5 10 15

Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys Ser Glu  
 20 25 30

Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile Asn Gly  
 35 40 45

Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser Asn Leu  
 50 55 60

Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met Lys Thr  
 65 70 75 80

Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr Leu Gly  
 85 90 95

Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile Asn Lys  
 100 105 110

Thr Ala Phe Glu Lys Ala Lys Phe Leu Asn Lys Asp Arg Leu  
 115 120 125

Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln Phe Ala  
 130 135 140

Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys Ala  
 145 150 155 160

Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met Leu  
 165 170 175

Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser Ser  
 180 185 190

Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala Ile  
 195 200 205

Asn Pro Lys  
 210

<210> 7  
 <211> 160  
 <212> PRT  
 <213> *Listeria monocytogenes*  
 <400> 7

Asn Lys Ser Leu Lys Phe Thr Ser Leu Glu Glu Ser Glu Lys Trp Gly  
 1 5 10 15

Ile Asp Gly Phe Ser Val Trp Arg Asn Ser Leu Ser Ser Arg Glu Ile  
 20 25 30

Gln Ala Ile Arg Asp Tyr Thr Asp Ile Trp His Tyr Gly Asn Met Asn  
 35 40 45

Gly Tyr Leu Arg Gly Ser Val Glu Lys Leu Ala Pro Asp Asn Ala Glu  
 50 55 60

Arg Ile Lys Asn Leu Ser Ser Ala Leu Glu Lys Ala Glu Leu Pro Asp  
 65 70 75 80

Asn Ile Ile Leu Tyr Arg Gly Thr Ser Ser Glu Ile Leu Asp Asn Phe  
 85 90 95

Leu Asp Leu Lys Asn Leu Asn Tyr Gln Asn Leu Val Gly Lys Thr Ile  
 100 105 110

Glu Glu Lys Gly Phe Met Ser Thr Thr Thr Ile Ser Asn Gln Thr Phe  
 115 120 125

Ser Gly Asn Val Thr Met Lys Ile Asn Ala Pro Lys Gly Ser Lys Gly  
 130 135 140

Ala Tyr Leu Ala His Phe Ser Glu Thr Pro Glu Glu Ala Glu Val Leu  
 145 150 155 160

<210> 8  
 <211> 175  
 <212> PRT  
 <213> *Clostridium acetobutylicum*  
 <400> 8

Thr Asn Met Asp Gln Ala Asn Glu Trp Gly Ser Gln Tyr Tyr Asp Asn  
 1 5 10 15

Trp Leu Lys Ser Leu Asn Asp Ser Glu Arg Asn Ala Ile Arg Gln Tyr  
 20 25 30

Thr Gly Asn Asp Tyr Lys Lys Ile Asn Asn Tyr Leu Arg Gly Val Asn  
 35 40 45

Asp Ser Leu Asp Gly Ile Asp Pro Lys Ile Ile Glu Asp Ile Lys Ser  
 50 55 60

Gly Leu Lys Lys Ala Ser Val Pro His Asp Met Lys Val Tyr Arg Gly  
 65 70 75 80

Thr Asp Leu Asn Pro Leu Arg Asn Leu Ile Asp Val Gly Lys Asp Gly  
 85 90 95

Ser Leu Asp Phe Ser Leu Val Gly Lys Thr Phe Lys Asp Asp Gly Phe  
 100 105 110

Met Ser Thr Ala Leu Val Lys Glu Ser Ser Phe Asp Tyr Met Asn Val  
 115 120 125

Ser Trp Glu Ile Asn Val Pro Lys Gly Thr Glu Ala Ala Tyr Val Ser  
 130 135 140

Lys Ile Ser Tyr Phe Pro Asp Glu Ala Glu Leu Leu Leu Asn His Gly  
 145 150 155 160

Gln Glu Met Ile Ile Lys Glu Ala Thr Val Gly Ser Asp Gly Lys  
 165 170 175

<210> 9  
 <211> 250  
 <212> PRT  
 <213> Streptococcus pyogenes  
 <400> 9

Met Leu Lys Lys Arg Tyr Gln Leu Ala Ile Val Leu Leu Leu Ser Cys  
 1 5 10 15

Phe Ser Leu Ile Trp Gln Thr Glu Gly Leu Val Glu Leu Phe Val Cys  
 20 25 30

Glu His Tyr Glu Arg Ala Val Cys Glu Gly Thr Pro Ala Tyr Phe Thr  
 35 40 45

Phe Ser Asp Gln Lys Gly Ala Glu Thr Leu Ile Lys Lys Arg Trp Gly  
 50 55 60

Lys Gly Leu Ile Tyr Pro Arg Ala Glu Gln Glu Ala Met Ala Ala Tyr  
 65 70 75 80

Thr Cys Gln Gln Ala Gly Pro Ile Asn Thr Ser Leu Asp Lys Ala Lys  
 85 90 95

Gly Glu Leu Ser Gln Leu Thr Pro Glu Leu Arg Asp Gln Val Ala Gln

100

105

110

Leu Asp Ala Ala Thr His Arg Leu Val Ile Pro Trp Asn Ile Val Val  
 115 120 125

Tyr Arg Tyr Val Tyr Glu Thr Phe Leu Arg Asp Ile Gly Val Ser His  
 130 135 140

Ala Asp Leu Thr Ser Tyr Tyr Arg Asn His Gln Phe Asp Pro His Ile  
 145 150 155 160

Leu Cys Lys Ile Lys Leu Gly Thr Arg Tyr Thr Lys His Ser Phe Met  
 165 170 175

Ser Thr Thr Ala Leu Lys Asn Gly Ala Met Thr His Arg Pro Val Glu  
 180 185 190

Val Arg Ile Cys Val Lys Lys Gly Ala Lys Ala Ala Phe Val Glu Pro  
 195 200 205

Tyr Ser Ala Val Pro Ser Glu Val Glu Leu Leu Phe Pro Arg Gly Cys  
 210 215 220

Gln Leu Glu Val Val Gly Ala Tyr Val Ser Gln Asp Gln Lys Lys Leu  
 225 230 235 240

His Ile Glu Ala Tyr Phe Lys Gly Ser Leu  
 245 250

<210> 10  
 <211> 250  
 <212> PRT  
 <213> Streptococcus pyogenes  
 <400> 10

Met Leu Lys Lys Arg Tyr Gln Leu Ala Ile Val Leu Leu Ser Cys  
 1 5 10 15

Phe Ser Leu Ile Trp Gln Thr Glu Gly Leu Val Glu Leu Phe Val Cys  
 20 25 30

Glu His Tyr Glu Arg Ala Val Cys Glu Gly Thr Pro Ala Tyr Phe Thr  
 35 40 45

Phe Ser Asp Gln Lys Gly Ala Glu Thr Leu Ile Lys Lys Arg Trp Gly  
 50 55 60

Lys Gly Leu Ile Tyr Pro Arg Ala Glu Gln Glu Ala Met Ala Ala Tyr  
 65 70 75 80

Thr Cys Gln Gln Ala Gly Pro Ile Asn Thr Ser Leu Asp Lys Ala Lys  
 85 90 95

Gly Glu Leu Ser Gln Leu Thr Pro Glu Leu Arg Asp Gln Val Ala Gln  
 100 105 110

Leu Asp Ala Ala Thr His Arg Leu Val Ile Pro Trp Asn Ile Val Val  
 115 120 125

Tyr Arg Tyr Val Tyr Glu Thr Phe Leu Arg Asp Ile Gly Val Ser His  
 130 135 140

Ala Asp Leu Thr Ser Tyr Tyr Arg Asn His Gln Phe Asp Pro His Ile  
 145 150 155 160

Leu Cys Lys Ile Lys Leu Gly Thr Arg Tyr Thr Lys His Ser Phe Met  
 165 170 175

Ser Thr Thr Ala Leu Lys Asn Gly Ala Met Thr His Arg Pro Val Glu  
 180 185 190

Val Arg Ile Cys Val Lys Lys Gly Ala Lys Ala Ala Phe Val Glu Pro  
 195 200 205

Tyr Ser Ala Val Pro Ser Glu Val Glu Leu Leu Phe Pro Arg Gly Cys  
 210 215 220

Gln Leu Glu Val Val Gly Ala Tyr Val Ser Gln Asp Gln Lys Lys Leu  
 225 230 235 240

His Ile Glu Ala Tyr Phe Lys Gly Ser Leu  
 245 250

<210> 11  
 <211> 855  
 <212> PRT  
 <213> Clostridium botulinum  
 <400> 11

Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn Lys Thr Leu Asp  
 1 5 10 15

Cys Arg Glu Leu Leu Val Lys Asn Thr Asp Leu Pro Phe Ile Gly Asp  
 20 25 30

Ile Ser Asp Val Lys Thr Asp Ile Phe Leu Arg Lys Asp Ile Asn Glu  
 35 40 45

Glu Thr Glu Val Ile Tyr Tyr Pro Asp Asn Val Ser Val Asp Gln Val

50

55

60

Ile Leu Ser Lys Asn Thr Ser Glu His Gly Gln Leu Asp Leu Leu Tyr  
 65 70 75 80

Pro Ser Ile Asp Ser Glu Ser Glu Ile Leu Pro Gly Glu Asn Gln Val  
 85 90 95

Phe Tyr Asp Asn Arg Thr Gln Asn Val Asp Tyr Leu Asn Ser Tyr Tyr  
 100 105 110

Tyr Leu Glu Ser Gln Lys Leu Ser Asp Asn Val Glu Asp Phe Thr Phe  
 115 120 125

Thr Arg Ser Ile Glu Glu Ala Leu Asp Asn Ser Ala Lys Val Tyr Thr  
 130 135 140

Tyr Phe Pro Thr Leu Ala Asn Lys Val Asn Ala Gly Val Gln Gly Gly  
 145 150 155 160

Leu Phe Leu Met Trp Ala Asn Asp Val Val Glu Asp Phe Thr Thr Asn  
 165 170 175

Ile Leu Arg Lys Asp Thr Leu Asp Lys Ile Ser Asp Val Ser Ala Ile  
 180 185 190

Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Ser Asn Ser Val Arg Arg  
 195 200 205

Gly Asn Phe Thr Glu Ala Phe Ala Val Thr Gly Val Thr Ile Leu Leu  
 210 215 220

Glu Ala Phe Pro Glu Phe Thr Ile Pro Ala Leu Gly Ala Phe Val Ile  
 225 230 235 240

Tyr Ser Lys Val Gln Glu Arg Asn Glu Ile Ile Lys Thr Ile Asp Asn  
 245 250 255

Cys Leu Glu Gln Arg Ile Lys Arg Trp Lys Asp Ser Tyr Glu Trp Met  
 260 265 270

Met Gly Thr Trp Leu Ser Arg Ile Ile Thr Gln Phe Asn Asn Ile Ser  
 275 280 285

Tyr Gln Met Tyr Asp Ser Leu Asn Tyr Gln Ala Gly Ala Ile Lys Ala  
 290 295 300

Lys Ile Asp Leu Glu Tyr Lys Lys Tyr Ser Gly Ser Asp Lys Glu Asn

305

310

315

320

Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu Asp Val Lys Ile  
 325 330 335

Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg Glu Cys Ser Val  
 340 345 350

Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile Asp Glu Leu Asn  
 355 360 365

Glu Phe Asp Arg Asn Thr Lys Ala Lys Leu Ile Asn Leu Ile Asp Ser  
 370 375 380

His Asn Ile Ile Leu Val Gly Glu Val Asp Lys Leu Lys Ala Lys Val  
 385 390 395 400

Asn Asn Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr  
 405 410 415

Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile  
 420 425 430

Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val  
 435 440 445

Asp Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln  
 450 455 460

Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu  
 465 470 475 480

Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn  
 485 490 495

Ser Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys  
 500 505 510

Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn  
 515 520 525

Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr  
 530 535 540

Leu Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp  
 545 550 555 560

Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val

565

570

575

Thr Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu  
 580 585 590

Ile Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys  
 595 600 605

Thr Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr  
 610 615 620

Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe  
 625 630 635 640

Ala Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu  
 645 650 655

Gln Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr  
 660 665 670

Asn Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met  
 675 680 685

Tyr Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn  
 690 695 700

Asp Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn  
 705 710 715 720

Thr Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met  
 725 730 735

Thr Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met  
 740 745 750

Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg  
 755 760 765

Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro  
 770 775 780

Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe  
 785 790 795 800

Asn Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe  
 805 810 815

Arg Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val

820

825

830

Lys Gln Gly Asn Tyr Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp  
 835 840 845

Gly Phe Val Pro Val Ser Glu  
 850 855

<210> 12  
 <211> 454  
 <212> PRT  
 <213> Clostridium botulinum  
 <400> 12

Gly Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn  
 1 5 10 15

Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn  
 20 25 30

Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp  
 35 40 45

Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu  
 50 55 60

Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp  
 65 70 75 80

Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser  
 85 90 95

Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp  
 100 105 110

Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn  
 115 120 125

Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu  
 130 135 140

Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile  
 145 150 155 160

Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr  
 165 170 175

Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile  
 180 185 190

Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr  
 195 200 205

Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser  
 210 215 220

Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala  
 225 230 235 240

Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln  
 245 250 255

Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn  
 260 265 270

Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr  
 275 280 285

Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp  
 290 295 300

Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr  
 305 310 315 320

Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr  
 325 330 335

Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr  
 340 345 350

Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu  
 355 360 365

Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met  
 370 375 380

Asn Asn Thr Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn  
 385 390 395 400

Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg  
 405 410 415

Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys  
 420 425 430

Gln Gly Asn Tyr Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly  
 435 440 445

Phe Val Pro Val Ser Glu  
450

<210> 13

<211> 1066

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 13

Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln Ala Lys  
1 5 10 15

Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys Ser Glu  
20 25 30

Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile Asn Gly  
35 40 45

Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser Asn Leu  
50 55 60

Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met Lys Thr  
65 70 75 80

Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr Leu Gly  
85 90 95

Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile Asn Lys  
100 105 110

Thr Ala Phe Glu Lys Ala Lys Phe Leu Asn Lys Asp Arg Leu  
115 120 125

Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln Phe Ala  
130 135 140

Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys Ala  
145 150 155 160

Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met Leu  
165 170 175

Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser Ser  
180 185 190

Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala Ile  
195 200 205

Asn Pro Lys Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn Lys  
 210 215 220

Thr Leu Asp Cys Arg Glu Leu Leu Val Lys Asn Thr Asp Leu Pro Phe  
 225 230 235 240

Ile Gly Asp Ile Ser Asp Val Lys Thr Asp Ile Phe Leu Arg Lys Asp  
 245 250 255

Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr Pro Asp Asn Val Ser Val  
 260 265 270

Asp Gln Val Ile Leu Ser Lys Asn Thr Ser Glu His Gly Gln Leu Asp  
 275 280 285

Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser Glu Ile Leu Pro Gly Glu  
 290 295 300

Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln Asn Val Asp Tyr Leu Asn  
 305 310 315 320

Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser Asp Asn Val Glu Asp  
 325 330 335

Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala Leu Asp Asn Ser Ala Lys  
 340 345 350

Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn Lys Val Asn Ala Gly Val  
 355 360 365

Gln Gly Gly Leu Phe Leu Met Trp Ala Asn Asp Val Val Glu Asp Phe  
 370 375 380

Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu Asp Lys Ile Ser Asp Val  
 385 390 395 400

Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Ser Asn Ser  
 405 410 415

Val Arg Arg Gly Asn Phe Thr Glu Ala Phe Ala Val Thr Gly Val Thr  
 420 425 430

Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr Ile Pro Ala Leu Gly Ala  
 435 440 445

Phe Val Ile Tyr Ser Lys Val Gln Glu Arg Asn Glu Ile Ile Lys Thr  
 450 455 460

Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys Arg Trp Lys Asp Ser Tyr  
 465 470 475 480 485 490 495  
 Glu Trp Met Met Gly Thr Trp Leu Ser Arg Ile Ile Thr Gln Phe Asn  
 495  
 Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu Asn Tyr Gln Ala Gly Ala  
 500 505 510  
 Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys Tyr Ser Gly Ser Asp  
 515 520 525  
 Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu Asp  
 530 535 540  
 Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg Glu  
 545 550 555 560  
 Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile Asp  
 565 570 575  
 Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys Ala Lys Leu Ile Asn Leu  
 580 585 590  
 Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu Val Asp Lys Leu Lys  
 595 600 605  
 Ala Lys Val Asn Asn Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile Phe  
 610 615 620  
 Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe  
 625 630 635 640  
 Asn Asn Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn  
 645 650 655  
 Thr Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly  
 660 665 670  
 Asp Val Gln Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser  
 675 680 685  
 Ser Gly Glu Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn Ile  
 690 695 700  
 Val Tyr Asn Ser Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg  
 705 710 715 720

Ile Asn Lys Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser  
 725 730 735

Val Lys Asn Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu  
 740 745 750

Val Phe Thr Leu Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe  
 755 760 765

Ser Tyr Asp Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe  
 770 775 780

Val Thr Val Thr Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile Asn  
 785 790 795 800

Gly Lys Leu Ile Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile Asn  
 805 810 815

Phe Ser Lys Thr Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly  
 820 825 830

Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp Phe  
 835 840 845

Tyr Ile Phe Ala Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe  
 850 855 860

Asn Ser Leu Gln Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn Asp  
 865 870 875 880

Leu Arg Tyr Asn Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn  
 885 890 895

Arg Tyr Met Tyr Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg Arg  
 900 905 910

Asn Asn Asn Asp Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile  
 915 920 925

Arg Gly Asn Thr Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr  
 930 935 940

Phe Asp Met Thr Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn  
 945 950 955 960

Glu Thr Met Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala Ile  
 965 970 975

Gly Leu Arg Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln  
 980 985 990

Ile Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys  
 995 1000 1005

Ser Asn Phe Asn Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile Gly  
 1010 1015 1020

Thr Tyr Arg Phe Arg Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr  
 1025 1030 1035

Leu Val Pro Thr Val Lys Gln Gly Asn Tyr Ala Ser Leu Leu Glu  
 1040 1045 1050

Ser Thr Ser Thr His Trp Gly Phe Val Pro Val Ser Glu  
 1055 1060 1065

<210> 14

<211> 1067

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 14

Ala Glu Thr Lys Asn Phe Thr Asp Leu Val Glu Ala Thr Lys Trp Gly  
 1 5 10 15

Asn Ser Leu Ile Lys Ser Ala Lys Tyr Ser Ser Lys Asp Lys Met Ala  
 20 25 30

Ile Tyr Asn Tyr Thr Lys Asn Ser Ser Pro Ile Asn Thr Pro Leu Arg  
 35 40 45

Ser Ala Asn Gly Asp Val Asn Lys Leu Ser Glu Asn Ile Gln Glu Gln  
 50 55 60

Val Arg Gln Leu Asp Ser Thr Ile Ser Lys Ser Val Thr Pro Asp Ser  
 65 70 75 80

Val Tyr Val Tyr Arg Leu Leu Asn Leu Asp Tyr Leu Ser Ser Ile Thr  
 85 90 95

Gly Phe Thr Arg Glu Asp Leu His Met Leu Gln Gln Thr Asn Asn Gly  
 100 105 110

Gln Tyr Asn Glu Ala Leu Val Ser Lys Leu Asn Asn Leu Met Asn Ser

115

120

125

Arg Ile Tyr Arg Glu Asn Gly Tyr Ser Ser Thr Gln Leu Val Ser Gly  
 130 135 140

Ala Ala Leu Ala Gly Arg Pro Ile Glu Leu Lys Leu Glu Leu Pro Lys  
 145 150 155 160

Gly Thr Lys Ala Ala Tyr Ile Asp Ser Lys Glu Leu Thr Ala Tyr Pro  
 165 170 175

Gly Gln Gln Glu Val Leu Leu Pro Arg Gly Thr Glu Tyr Ala Val Gly  
 180 185 190

Ser Val Lys Leu Ser Asp Asn Lys Arg Lys Ile Ile Ile Thr Ala Val  
 195 200 205

Val Phe Lys Lys Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn  
 210 215 220

Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys Asn Thr Asp Leu Pro  
 225 230 235 240

Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp Ile Phe Leu Arg Lys  
 245 250 255

Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr Pro Asp Asn Val Ser  
 260 265 270

Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser Glu His Gly Gln Leu  
 275 280 285

Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser Glu Ile Leu Pro Gly  
 290 295 300

Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln Asn Val Asp Tyr Leu  
 305 310 315 320

Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser Asp Asn Val Glu  
 325 330 335

Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala Leu Asp Asn Ser Ala  
 340 345 350

Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn Lys Val Asn Ala Gly  
 355 360 365

Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn Asp Val Val Glu Asp

370

375

380

Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu Asp Lys Ile Ser Asp  
 385 390 395 400

Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Ser Asn  
 405 410 415

Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe Ala Val Thr Gly Val  
 420 425 430

Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr Ile Pro Ala Leu Gly  
 435 440 445

Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg Asn Glu Ile Ile Lys  
 450 455 460

Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys Arg Trp Lys Asp Ser  
 465 470 475 480

Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg Ile Ile Thr Gln Phe  
 485 490 495

Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu Asn Tyr Gln Ala Gly  
 500 505 510

Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys Tyr Ser Gly Ser  
 515 520 525

Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu  
 530 535 540

Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg  
 545 550 555 560

Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile  
 565 570 575

Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys Ala Lys Leu Ile Asn  
 580 585 590

Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu Val Asp Lys Leu  
 595 600 605

Lys Ala Lys Val Asn Asn Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile  
 610 615 620

Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr

625

630

635

640

Phe Asn Asn Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys  
 645 650 655

Asn Thr Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu  
 660 665 670

Gly Asp Val Gln Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly  
 675 680 685

Ser Ser Gly Glu Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn  
 690 695 700

Ile Val Tyr Asn Ser Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile  
 705 710 715 720

Arg Ile Asn Lys Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp  
 725 730 735

Ser Val Lys Asn Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe  
 740 745 750

Leu Val Phe Thr Leu Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn  
 755 760 765

Phe Ser Tyr Asp Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe  
 770 775 780

Phe Val Thr Val Thr Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile  
 785 790 795 800

Asn Gly Lys Leu Ile Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile  
 805 810 815

Asn Phe Ser Lys Thr Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr  
 820 825 830

Gly Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp  
 835 840 845

Phe Tyr Ile Phe Ala Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu  
 850 855 860

Phe Asn Ser Leu Gln Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn  
 865 870 875 880

Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu

885

890

895

Asn Arg Tyr Met Tyr Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg  
 900 905 910

Arg Asn Asn Asn Asp Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg  
 915 920 925

Ile Arg Gly Asn Thr Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu  
 930 935 940

Tyr Phe Asp Met Thr Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys  
 945 950 955 960

Asn Glu Thr Met Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala  
 965 970 975

Ile Gly Leu Arg Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe  
 980 985 990

Gln Ile Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe  
 995 1000 1005

Lys Ser Asn Phe Asn Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile  
 1010 1015 1020

Gly Thr Tyr Arg Phe Arg Leu Gly Gly Asp Trp Tyr Arg His Asn  
 1025 1030 1035

Tyr Leu Val Pro Thr Val Lys Gln Gly Asn Tyr Ala Ser Leu Leu  
 1040 1045 1050

Glu Ser Thr Ser Thr His Trp Gly Phe Val Pro Val Ser Glu  
 1055 1060 1065

<210> 15

<211> 682

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 15

Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln Ala Lys  
 1 5 10 15

Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys Ser Glu  
 20 25 30

Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile Asn Gly  
 35 40 45

Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser Asn Leu  
 50 55 60

Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met Lys Thr  
 65 70 75 80

Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr Leu Gly  
 85 90 95

Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile Asn Lys  
 100 105 110

Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp Arg Leu  
 115 120 125

Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln Phe Ala  
 130 135 140

Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys Ala  
 145 150 155 160

Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met Leu  
 165 170 175

Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser Ser  
 180 185 190

Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala Ile  
 195 200 205

Asn Pro Lys Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn Lys  
 210 215 220

Thr Leu Asp Cys Gly Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile Phe  
 225 230 235 240

Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe  
 245 250 255

Asn Asn Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn  
 260 265 270

Thr Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly  
 275 280 285

Asp Val Gln Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser  
 290 295 300  
  
 Ser Gly Glu Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn Ile  
 305 310 315 320  
  
 Val Tyr Asn Ser Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg  
 325 330 335  
  
 Ile Asn Lys Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser  
 340 345 350  
  
 Val Lys Asn Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu  
 355 360 365  
  
 Val Phe Thr Leu Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe  
 370 375 380  
  
 Ser Tyr Asp Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe  
 385 390 395 400  
  
 Val Thr Val Thr Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile Asn  
 405 410 415  
  
 Gly Lys Leu Ile Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile Asn  
 420 425 430  
  
 Phe Ser Lys Thr Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly  
 435 440 445  
  
 Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp Phe  
 450 455 460  
  
 Tyr Ile Phe Ala Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe  
 465 470 475 480  
  
 Asn Ser Leu Gln Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn Asp  
 485 490 495  
  
 Leu Arg Tyr Asn Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn  
 500 505 510  
  
 Arg Tyr Met Tyr Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg Arg  
 515 520 525  
  
 Asn Asn Asn Asp Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile  
 530 535 540

Arg Gly Asn Thr Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr  
 545 550 555 560

Phe Asp Met Thr Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn  
 565 570 575

Glu Thr Met Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala Ile  
 580 585 590

Gly Leu Arg Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln  
 595 600 605

Ile Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys  
 610 615 620

Ser Asn Phe Asn Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr  
 625 630 635 640

Tyr Arg Phe Arg Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr Leu Val  
 645 650 655

Pro Thr Val Lys Gln Gly Asn Tyr Ala Ser Leu Leu Glu Ser Thr Ser  
 660 665 670

Thr His Trp Gly Phe Val Pro Val Ser Glu  
 675 680

<210> 16

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 16

Cys Ser Ala Ile Glu Gly Arg Ala Pro Gly Ile Cys  
 1 5 10

<210> 17

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 17

Cys Gly Ile Glu Gly Arg Ala Pro Gly Pro Gly Ser Ser Val Gly Ser  
 1 5 10 15

Ser Leu Ser Cys  
 20

<210> 18

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 18

Cys Gly Leu Val Pro Arg Gly Ser Gly Pro Cys  
1 5 10

<210> 19

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 19

Cys Gly Leu Val Pro Arg Gly Ser Gly Pro Gly Ser Ser Val Gly Ser  
1 5 10 15

Ser Leu Ser Cys  
20

<210> 20

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 20

Cys Lys Ser Asp Asp Asp Asp Lys Ala Pro Gly Ile Cys  
1 5 10

<210> 21

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 21

Cys Lys Ser Glu Glu Lys Leu Tyr Asp Asp Asp Asp Lys Asp Arg Trp  
1 5 10 15

Gly Ser Ser Arg Ile Cys  
20

<210> 22

<211> 17

<212> PRT  
<213> Clostridium Botulinum  
<400> 22

Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn Lys Thr Leu Asp  
1 5 10 15

Cys

<210> 23  
<211> 10  
<212> PRT  
<213> Artificial Sequence  
<220>  
<223> Synthetic

<400> 23

Cys Gly Leu Val Pro Ala Gly Ser Gly Pro  
1 5 10

<210> 24  
<211> 17  
<212> PRT  
<213> Artificial Sequence  
<220>  
<223> Synthetic

<400> 24

Cys Gly Leu Val Pro Ala Gly Ser Gly Pro Ser Ala Gly Ser Ser Ala  
1 5 10 15

Cys

<210> 25  
<211> 10  
<212> PRT  
<213> Artificial Sequence  
<220>  
<223> Synthetic

<400> 25

Gly Gly Gly Gly Ser Gly Gly Gly Ser  
1 5 10

<210> 26  
<211> 15  
<212> PRT  
<213> Artificial Sequence  
<220>  
<223> Synthetic

<400> 26

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
1 5 10 15

<210> 27

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 27

Pro Pro Pro Ile Glu Gly Arg  
1 5

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re Application of: )  
Clifford Charles Shone et al. )  
International Application No. PCT/GB03/03082 ) Examiner: Brian J. Gangle  
Application No.: 10/521,401 ) Group Art Unit: 1645  
International Filing Date: July 15, 2003 ) Confirmation No.: 2849

For **TARGETED AGENTS FOR NERVE  
REGENERATION**

**STATEMENT ACCORDING TO 37 C.F.R. § 1.821(f)**

M.S. – SEQUENCE LISTING  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

Dear Sir:

Submitted herewith is a sequence listing as part of the above-captioned patent application. Applicants' representative states that the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 CFR 1.821(c) and (e), respectively, are identical.

Applicants' representative hereby verifies that the information on the accompanying computer readable copy is identical to the paper copy of the sequence listing. The enclosed sequence listing does not include any new matter that goes beyond the disclosure in the above-captioned application as filed.

Respectfully submitted,

  
Daniel W. Celander, Ph.D.  
Registration No. 52,710

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